

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/095,478

DATE: 06/17/98
TIME: 10:45:42

INPUT SET: S26785.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

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(1) General Information:

ENTERED

(i) APPLICANT: Plowman, Gregory

(ii) TITLE OF INVENTION: NOVEL PROTEIN TYROSINE
PHOSPHATASE SuPTP05 AND
RELATED PRODUCTS AND
METHODS

(iii) NUMBER OF SEQUENCES: 25

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon
(B) STREET: 633 West Fifth Street
Suite 4700
(C) CITY: Los Angeles
(D) STATE: California
(E) COUNTRY: U.S.A.
(F) ZIP: 90071-2066

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0
(D) SOFTWARE: FastSEQ for Windows 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:

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47 (B) FILING DATE:
48
4950 (viii) ATTORNEY/AGENT INFORMATION:
5152 (A) NAME: Warburg, Richard J.
53 (B) REGISTRATION NUMBER: 32,327
54 (C) REFERENCE/DOCKET NUMBER: 224/115
55
5657 (ix) TELECOMMUNICATION INFORMATION:
5859 (A) TELEPHONE: (213) 489-1600
60 (B) TELEFAX: (213) 955-0440
61 (C) TELEX: 67-3510
62
63
6465 (2) INFORMATION FOR SEQ ID NO: 1:
6667 (i) SEQUENCE CHARACTERISTICS:
6869 (A) LENGTH: 426 amino acids
70 (B) TYPE: amino acid
71 (C) STRANDEDNESS: single
72 (D) TOPOLOGY: linear
7374 (ii) MOLECULE TYPE: Peptide
7576 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
7778 Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
79 1 5 10 15
8081 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
82 20 25 30
8384 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Ile Phe Gly Asn Lys
85 35 40 45
8687 Met Asn Ser Glu Asn Val Lys Pro Ser His His Leu Ser Phe Ser Asp
88 50 55 60
8990 Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu Ser Asp Thr Asp Glu
91 65 70 75 80
9293 Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg Asn Arg Trp Asn Ser
94 85 90 95
9596 Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr Val Ser Pro Val Leu
97 100 105 110
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99 Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu Thr Ser Val Ser Glu

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100	115	120	125
101			
102	Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro Leu Ile Phe Asn Ser		
103	130	135	140
104			
105	Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn Thr Leu Gln Lys Lys		
106	145	150	155
107			
108	Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu Leu Glu Gln Met Thr		
109		165	170
110			175
111	Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu Gln Asn Arg Asp Lys		
112	180	185	190
113			
114	Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser Thr Arg Val Pro Leu		
115	195	200	205
116			
117	Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr Ile Arg Ile Val Asn		
118	210	215	220
119			
120	His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln Gly Pro Leu Pro Glu		
121	225	230	235
122			
123	Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu Asn Asn Cys Asn Val		
124		245	250
125			255
126	Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly Val Ile Lys Cys Tyr		
127	260	265	270
128			
129	Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu Glu Phe Glu His Phe		
130	275	280	285
131			
132	Ser Val Phe Leu Glu Thr Phe His Val Thr Gln Tyr Phe Thr Val Arg		
133	290	295	300
134			
135	Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys Ser Gln Cys Val Lys		
136	305	310	315
137			
138	His Leu Gln Phe Thr Lys Trp Pro Asp His Gly Thr Pro Ala Ser Ala		
139		325	330
140			335
141	Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg Lys Ser His Ile Thr		
142		340	345
143			350
144	Gly Pro Leu Leu Val His Cys Ser Ala Gly Val Gly Arg Thr Gly Val		
145	355	360	365
146			
147	Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile Glu Lys Asn Tyr Ser		
148	370	375	380
149			
150	Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg Lys Gln Arg Cys Gly		
151	385	390	395
152			400

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153 Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys Tyr Glu Ile Val Leu
154 405 410 415

155
156 Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr
157 420 425
158
159
160

161 (2) INFORMATION FOR SEQ ID NO: 2:
162

163 (i) SEQUENCE CHARACTERISTICS:
164

165 (A) LENGTH: 463 amino acids
166 (B) TYPE: amino acid
167 (C) STRANDEDNESS: single
168 (D) TOPOLOGY: linear
169

170 (ii) MOLECULE TYPE: Peptide
171

172 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
173

174 Met Ser Ser Pro Arg Lys Val Arg Gly Lys Thr Gly Arg Asp Asn Asp
175 1 5 10 15
176

177 Glu Glu Glu Gly Asn Ser Gly Asn Leu Asn Leu Arg Asn Ser Leu Pro
178 20 25 30
179

180 Ser Ser Ser Gln Lys Met Thr Pro Thr Lys Pro Val Gln Asn Lys Asn
181 35 40 45
182

183 Leu Met Lys Tyr Glu Glu His Leu Asp Ile Leu Met Val Phe Leu Leu
184 50 55 60
185

186 Ile Lys Thr Ile Trp Tyr Asn Val Phe Lys Leu Trp Lys Gly Lys Leu
187 65 70 75 80
188

189 Ile Phe Gly Asn Lys Met Asn Ser Glu Asn Val Lys Pro Ser His His
190 85 90 95
191

192 Leu Ser Phe Ser Asp Lys Tyr Glu Leu Val Tyr Pro Glu Pro Leu Glu
193 100 105 110
194

195 Ser Asp Thr Asp Glu Thr Val Trp Asp Val Ser Asp Arg Ser Leu Arg
196 115 120 125
197

198 Asn Arg Trp Asn Ser Met Asp Ser Glu Thr Ala Gly Pro Ser Lys Thr
199 130 135 140
200

201 Val Ser Pro Val Leu Ser Gly Ser Ser Arg Leu Ser Lys Asp Thr Glu
202 145 150 155 160
203

204 Thr Ser Val Ser Glu Lys Glu Leu Thr Gln Leu Ala Gln Ile Arg Pro
205 165 170 175

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206
207   Leu Ile Phe Asn Ser Ser Ala Arg Ser Ala Met Arg Asp Cys Leu Asn
208               180               185               190
209
210   Thr Leu Gln Lys Lys Glu Glu Leu Asp Ile Ile Arg Glu Phe Leu Glu
211               195               200               205
212
213   Leu Glu Gln Met Thr Leu Pro Asp Asp Phe Asn Ser Gly Asn Thr Leu
214               210               215               220
215
216   Gln Asn Arg Asp Lys Asn Arg Tyr Arg Asp Ile Leu Pro Tyr Asp Ser
217   225               230               235               240
218
219   Thr Arg Val Pro Leu Gly Lys Asn Lys Asp Tyr Ile Asn Ala Ser Tyr
220               245               250               255
221
222   Ile Arg Ile Val Asn His Glu Glu Glu Tyr Phe Tyr Ile Ala Thr Gln
223               260               265               270
224
225   Gly Pro Leu Pro Glu Thr Ile Glu Asp Phe Trp Gln Met Val Leu Glu
226               275               280               285
227
228   Asn Asn Cys Asn Val Ile Ala Met Ile Thr Arg Glu Ile Glu Cys Gly
229   290               295               300
230
231   Val Ile Lys Cys Tyr Ser Tyr Trp Pro Ile Ser Leu Lys Glu Pro Leu
232   305               310               315               320
233
234   Glu Phe Glu His Phe Ser Val Phe Leu Glu Thr Phe His Val Thr Gln
235               325               330               335
236
237   Tyr Phe Thr Val Arg Val Phe Gln Ile Val Lys Lys Ser Thr Gly Lys
238               340               345               350
239
240   Ser Gln Cys Val Lys His Leu Gln Phe Thr Lys Trp Pro Asp His Gly
241               355               360               365
242
243   Thr Pro Ala Ser Ala Asp Phe Phe Ile Lys Tyr Val Arg Tyr Val Arg
244               370               375               380
245
246   Lys Ser His Ile Thr Gly Pro Leu Leu Val His Cys Ser Ala Gly Val
247   385               390               395               400
248
249   Gly Arg Thr Gly Val Phe Ile Cys Val Asp Val Val Phe Ser Ala Ile
250               405               410               415
251
252   Glu Lys Asn Tyr Ser Phe Asp Ile Met Asn Ile Val Thr Gln Met Arg
253               420               425               430
254
255   Lys Gln Arg Cys Gly Met Ile Gln Thr Lys Glu Gln Tyr Gln Phe Cys
256               435               440               445
257
258   Tyr Glu Ile Val Leu Glu Val Leu Gln Asn Leu Leu Ala Leu Tyr

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SEQUENCE VERIFICATION REPORT
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Error

Original Text